RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _O9/840,277A_

Source: _1600_

Date Processed by STIC: _9/28/2003_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 4.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
<u>http://www.uspto.gov/web/offices/pac/checker</u>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<u><http://www.uspto.gov/ebc/efs/downloads/documents.htm></u> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to:
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
          Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003

ERROR DETECTED **SUGGESTED CORRECTION** SERIAL NUMBER: _09/840,277A_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino
Numbering

The numbering under each 5ᵗʰ amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ✓ Variable Length

Sequence(s)__14__ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)_____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7____Skipped Sequences
(OLD RULES)

Sequence(s)_____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences
(NEW RULES)

Sequence(s)_10_ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10____Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11____Use of <220>

Sequence(s)_____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

1600

```
RAW SEQUENCE LISTING              DATE: 07/28/2003
PATENT APPLICATION:  US/09/840,277A      TIME: 09:45:54

Input Set : A:\A-688A.ST25.txt
Output Set: N:\CRF4\07282003\I840277A.raw

 3 <110> APPLICANT: FEIGE, ULRICH
 4        KOHNO, TADAHIKO
 5        LACEY, DAVID
 6        BOONE, THOMAS CHARLES
 8 <120> TITLE OF INVENTION: ADHESION ANTAGONISTS (as amended)
10 <130> FILE REFERENCE: A-688A
12 <140> CURRENT APPLICATION NUMBER: US 09/840,277A
13 <141> CURRENT FILING DATE: 2003-04-23
15 <150> PRIOR APPLICATION NUMBER: US 60/198,919
16 <151> PRIOR FILING DATE: 2000-04-21
18 <150> PRIOR APPLICATION NUMBER: US 60/201,394
19 <151> PRIOR FILING DATE: 2000-05-03
21 <160> NUMBER OF SEQ ID NOS: 135
23 <170> SOFTWARE: PatentIn version 3.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 684
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1)..(684)
33 <223> OTHER INFORMATION:
36 <400> 1
37 atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg      48
38 Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
39 1               5                   10                  15
41 ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc      96
42 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
43              20                  25                  30
45 atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc     144
46 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
47          35                  40                  45
49 cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag     192
50 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
51      50                  55                  60
53 gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg     240
54 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
55 65                  70                  75                  80
57 tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat     288
58 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
59                  85                  90                  95
61 ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc     336
62 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
```

Does Not Comply
Corrected Diskette Needed

```
63                 100                 105                 110
65 atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag       384
66 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
67     115                 120                 125
69 gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc       432
70 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
71     130                 135                 140
73 agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg       480
74 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
75 145                 150                 155                 160
77 gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct       528
78 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
79                 165                 170                 175
81 ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc       576
82 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
83                 180                 185                 190
85 gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg       624
86 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
87                 195                 200                 205
89 atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg       672
90 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
91     210                 215                 220
93 tct ccg ggt aaa                                                       684
94 Ser Pro Gly Lys
95 225
98 <210> SEQ ID NO: 2
99 <211> LENGTH: 228
100 <212> TYPE: PRT
101 <213> ORGANISM: Homo sapiens
103 <400> SEQUENCE: 2
105 Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
106 1               5                   10                  15
109 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
110             20                  25                  30
113 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
114         35                  40                  45
117 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
118     50                  55                  60
121 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
122 65                  70                  75                  80
125 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
126             85                  90                  95
129 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
130             100                 105                 110
133 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
134     115                 120                 125
137 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
138     130                 135                 140
141 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
```

```
142 145                    150                  155                      160
145 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
146              165                  170                      175
149 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
150              180                  185                      190
153 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
154          195                  200                      205
157 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
158      210                  215                      220
161 Ser Pro Gly Lys
162 225
165 <210> SEQ ID NO: 3
166 <211> LENGTH: 8
167 <212> TYPE: PRT
168 <213> ORGANISM: Artificial Sequence
170 <220> FEATURE:
171 <223> OTHER INFORMATION: Preferred linker
173 <400> SEQUENCE: 3
175 Gly Gly Gly Lys Gly Gly Gly Gly
176 1               5
179 <210> SEQ ID NO: 4
180 <211> LENGTH: 8
181 <212> TYPE: PRT
182 <213> ORGANISM: Artificial Sequence
184 <220> FEATURE:
185 <223> OTHER INFORMATION: Preferred linker
187 <400> SEQUENCE: 4
189 Gly Gly Gly Asn Gly Ser Gly Gly
190 1               5
193 <210> SEQ ID NO: 5
194 <211> LENGTH: 8
195 <212> TYPE: PRT
196 <213> ORGANISM: Artificial Sequence
198 <220> FEATURE:
199 <223> OTHER INFORMATION: Preferred linker
201 <400> SEQUENCE: 5
203 Gly Gly Gly Cys Gly Gly Gly Gly
204 1               5
207 <210> SEQ ID NO: 6
208 <211> LENGTH: 5
209 <212> TYPE: PRT
210 <213> ORGANISM: Artificial Sequence
212 <220> FEATURE:
213 <223> OTHER INFORMATION: Preferred linker
215 <400> SEQUENCE: 6
217 Gly Pro Asn Gly Gly
218 1               5
221 <210> SEQ ID NO: 7
222 <211> LENGTH: 5
```

```
223 <212> TYPE: PRT
224 <213> ORGANISM: Artificial Sequence
226 <220> FEATURE:
227 <223> OTHER INFORMATION: Laminin peptide
229 <400> SEQUENCE: 7
231 Tyr Ile Gly Ser Arg
232 1               5
235 <210> SEQ ID NO: 8
236 <211> LENGTH: 49
237 <212> TYPE: PRT
238 <213> ORGANISM: Artificial Sequence
240 <220> FEATURE:
241 <223> OTHER INFORMATION: Echistatin peptide
243 <400> SEQUENCE: 8
245 Glu Cys Glu Ser Gly Pro Cys Cys Arg Asn Cys Lys Phe Leu Lys Glu
246 1               5               10              15
249 Gly Thr Ile Cys Lys Arg Ala Arg Gly Asp Asp Met Asp Asp Tyr Cys
250             20              25              30
253 Asn Gly Lys Thr Cys Asp Cys Pro Arg Asn Pro His Lys Gly Pro Ala
254         35              40              45
257 Thr
261 <210> SEQ ID NO: 9
262 <211> LENGTH: 7
263 <212> TYPE: PRT
264 <213> ORGANISM: Artificial Sequence
266 <220> FEATURE:
267 <223> OTHER INFORMATION: RGD, NGR derivative peptide
269 <220> FEATURE:
270 <221> NAME/KEY: misc_feature
271 <222> LOCATION: (2, 5 and)..(7)
272 <223> OTHER INFORMATION: Xaa is any amino acid
275 <400> SEQUENCE: 9
```
W--> **277 Arg Xaa Glu Thr Xaa Trp Xaa**
```
278 1               5
281 <210> SEQ ID NO: 10
282 <211> LENGTH: 0
283 <212> TYPE: PRT
284 <213> ORGANISM: Deleted Sequence
286 <400> SEQUENCE: 10
```
W--> **287 000**
```
288 <210> SEQ ID NO: 11
289 <211> LENGTH: 9
290 <212> TYPE: PRT
291 <213> ORGANISM: Artificial Sequence
293 <220> FEATURE:
294 <223> OTHER INFORMATION: RGD, NGR derivative peptide
296 <220> FEATURE:
297 <221> NAME/KEY: misc_feature
298 <222> LOCATION: (2, 3, 7 and)..(8)
```

delete this - these lines are not needed in an intentionally skipped sequence (see item 8 on Error Summary Sheet)

RAW SEQUENCE LISTING   DATE: 07/28/2003
PATENT APPLICATION: US/09/840,277A   TIME: 09:45:54

Input Set : A:\A-688A.ST25.txt
Output Set: N:\CRF4\07282003\I840277A.raw

```
      299 <223> OTHER INFORMATION: Xaa is any amino acid
      302 <400> SEQUENCE: 11
W--> 304 Cys Xaa Xaa Arg Leu Asp Xaa Xaa Cys
      305 1               5
      308 <210> SEQ ID NO: 12
      309 <211> LENGTH: 7
      310 <212> TYPE: PRT
      311 <213> ORGANISM: Artificial Sequence
      313 <220> FEATURE:
      314 <223> OTHER INFORMATION: RGD, NGR derivative peptide
      316 <220> FEATURE:
      317 <221> NAME/KEY: misc_feature
      318 <222> LOCATION: (2 and)..(3)
      319 <223> OTHER INFORMATION: Xaa is any amino acid
      322 <400> SEQUENCE: 12
W--> 324 Cys Xaa Xaa Arg Gly Asp Cys
      325 1               5
      328 <210> SEQ ID NO: 13
      329 <211> LENGTH: 9
      330 <212> TYPE: PRT
      331 <213> ORGANISM: Artificial Sequence
      333 <220> FEATURE:
      334 <223> OTHER INFORMATION: RGD, NGR derivative peptide
      336 <220> FEATURE:
      337 <221> NAME/KEY: misc_feature
      338 <222> LOCATION: (1, 2, 3, 7, 8 and)...(9)
      339 <223> OTHER INFORMATION: Xaa is any amino acid with Xaa at 1, 3, 7 and 9 capable of
formin
      340        g a bridge.
      343 <400> SEQUENCE: 13
W--> 345 Xaa Xaa Xaa Arg Gly Asp Xaa Xaa Xaa
      346 1               5
      349 <210> SEQ ID NO: 14
      350 <211> LENGTH: 9
      351 <212> TYPE: PRT
      352 <213> ORGANISM: Artificial Sequence
      354 <220> FEATURE:
      355 <223> OTHER INFORMATION: RGD, NGR derivative peptide
      357 <220> FEATURE:
      358 <221> NAME/KEY: misc_feature
      359 <222> LOCATION: (2 )..(8)
      360 <223> OTHER INFORMATION: Xaa is 1 to 5 amino acids.
      364 <400> SEQUENCE: 14
W--> 366 Cys Xaa Cys Arg Gly Asp Cys Xaa Cys
      367 1               5
      370 <210> SEQ ID NO: 15
      371 <211> LENGTH: 8
      372 <212> TYPE: PRT
      373 <213> ORGANISM: Artificial Sequence
      375 <220> FEATURE:
```

Xaa can only represent one amino acid (see item 5 on Error Summary Sheet) (handwritten annotation)

RAW SEQUENCE LISTING ERROR SUMMARY   `DATE: 07/28/2003`
PATENT APPLICATION: **US/09/840,277A**   TIME: 09:45:55

Input Set : **A:\A-688A.ST25.txt**
Output Set: **N:\CRF4\07282003\I840277A.raw**

<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

```
Seq#:9;  Xaa Pos. 2,5,7
Seq#:11; Xaa Pos. 2,3,7,8
Seq#:12; Xaa Pos. 2,3
Seq#:13; Xaa Pos. 1,2,3,7,8,9
Seq#:14; Xaa Pos. 2,8
Seq#:15; Xaa Pos. 1,2,5,6,7,8
Seq#:16; Xaa Pos. 1,2,3,6,7,8,9,10
Seq#:17; Xaa Pos. 3,5,6,13,15
Seq#:18; Xaa Pos. 2,3,4,7,15
Seq#:19; Xaa Pos. 3,4,5,6,8,13,15,18
Seq#:20; Xaa Pos. 2,5,6,7,12,13,14
Seq#:21; Xaa Pos. 1,3,6,9,12,13
Seq#:40; Xaa Pos. 3,4
Seq#:50; Xaa Pos. 2,3
Seq#:58; Xaa Pos. 5
Seq#:59; Xaa Pos. 6
Seq#:86; Xaa Pos. 3,15
Seq#:87; Xaa Pos. 13,15
```

VERIFICATION SUMMARY　　　　　　　　　DATE: 07/28/2003
PATENT APPLICATION: **US/09/840,277A**　　TIME: 09:45:55

Input Set : **A:\A-688A.ST25.txt**
Output Set: **N:\CRF4\07282003\I840277A.raw**

```
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:36 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:33
L:277 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:287 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (10) SEQUENCE:
L:304 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:345 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:366 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:406 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:459 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
L:479 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:503 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
L:523 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
M:341 Repeated in SeqNo=19
L:547 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0
L:567 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0
L:839 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:0
L:985 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50 after pos.:0
L:1131 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:0
L:1151 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59 after pos.:0
L:1547 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86 after pos.:0
L:1567 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:87 after pos.:0
L:1889 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:108,Line#:1880
```